

SEQUENCE LISTING



<110> LEUNG, Shui-on
HANSEN, Hans

<120> IMMUNOCONJUGATES AND HUMANIZED ANTIBODIES SPECIFIC FOR B-CELL
LYMPHOMA AND LEUKEMIA CELLS

<130> 18733/1082

<140> US 09/988,013

<141> 2001-11-16

<150> US 09/741,843

<151> 2000-12-22

<150> US 09/127,902

<151> 1998-08-03

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<151> 1996-07-06

<150> US 08/289,576

<151> 1994-08-12

<160> 25

<170> PatentIn version 3.1

<210> 1

<211> 339

<212> DNA

<213> Murinae gen. sp.

<220>

<221> CDS

<222> (1)..(339)

<223>

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 gaa aac gtc act atg agc tgt aag tcc agt caa agt gtt tta tac agt	96
Glu Asn Val Thr Met Ser Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser	
20 25 30	
 gca aat cac aag aac tac ttg gcc tgg tac cag cag aaa cca ggg cag	144
Ala Asn His Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln	
35 40 45	
 tct cct aaa ctg ctg atc tac tgg gca tcc act agg gaa tct ggt gtc	192
Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val	
50 55 60	

cct gat cgc ttc aca ggc agc gga tct ggg aca gat ttt act ctt acc 240
 Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 65 70 75 80

atc agc aga gta caa gtt gaa gac ctg gca att tat tat tgt cac caa 288
 Ile Ser Arg Val Gln Val Glu Asp Leu Ala Ile Tyr Tyr Cys His Gln
 85 90 95

tac ctc tcc tcg tgg acg ttc ggt gga ggg acc aag ctg gag atc aaa 336
 Tyr Leu Ser Ser Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105 110

cgt 339
 Arg

<210> 2
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 <212> PRT
 <213> Murinae gen. sp.

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Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ala Val Ser Ala Gly
 1 5 10 15

Glu Asn Val Thr Met Ser Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
 20 25 30

Ala Asn His Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
 35 40 45

Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
 50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 65 70 75 80

Ile Ser Arg Val Gln Val Glu Asp Leu Ala Ile Tyr Tyr Cys His Gln
 85 90 95

Tyr Leu Ser Ser Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105 110

Arg

<210> 3
 <211> 348
 <212> DNA
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 1 5 10 15
 tca gtg aag atg tcc tgc aag gct tct ggc tac acc ttt act agc tac 96
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 20 25 30
 tgg ctg cac tgg ata aaa cag agg cct gga cag ggt ctg gaa tgg att 144
 Trp Leu His Trp Ile Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45
 gga tac att aat cct agg aat gat tat act gag tac aat cag aac ttc 192
 Gly Tyr Ile Asn Pro Arg Asn Asp Tyr Thr Glu Tyr Asn Gln Asn Phe
 50 55 60
 aag gac aag gcc aca ttg act gca gac aaa tcc tcc agc aca gcc tac 240
 Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80
 atg caa ctg agc agc ctg aca tct gag gac tct gca gtc tat tac tgt 288
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
 85 90 95
 gca aga agg gat att act acg ttc tac tgg ggc caa ggc acc act ctc 336
 Ala Arg Arg Asp Ile Thr Thr Phe Tyr Trp Gly Gln Gly Thr Thr Leu
 100 105 110
 aca gtc tcc tcg 348
 Thr Val Ser Ser
 115

<210> 4
 <211> 116
 <212> PRT
 <213> Murinae gen. sp.

<400> 4
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 1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 20 25 30

Trp Leu His Trp Ile Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Tyr Ile Asn Pro Arg Asn Asp Tyr Thr Glu Tyr Asn Gln Asn Phe
 50 55 60

Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Arg Asp Ile Thr Thr Phe Tyr Trp Gly Gln Gly Thr Thr Leu
 100 105 110

Thr Val Ser Ser
 115

<210> 5
 <211> 339
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (1)..(339)
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gat agg gtc act atg agc tgt aag tcc agt caa agt gtt tta tac agt 96
 Asp Arg Val Thr Met Ser Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
 20 25 30

gca aat cac aag aac tac ttg gcc tgg tac cag cag aaa cca ggg aaa 144
 Ala Asn His Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
 35 40 45

gca cct aaa ctg ctg atc tac tgg gca tcc act agg gaa tct ggt gtc 192
 Ala Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
 50 55 60

cct	tcg	cga	ttc	tct	ggc	agc	gga	tct	ggg	aca	gat	ttt	act	ttc	acc	240
Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Phe	Thr	
65					70					75					80	

atc	agc	tct	ctt	caa	cca	gaa	gac	att	gca	aca	tat	tat	tgt	cac	caa	288
Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	Ile	Ala	Thr	Tyr	Tyr	Cys	His	Gln	
				85					90					95		

tac	ctc	tcc	tcg	tgg	acg	ttc	ggg	gga	ggg	acc	aag	gtg	cag	atc	aaa	336
Tyr	Leu	Ser	Ser	Trp	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Gln	Ile	Lys	
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cgt																339
Arg																

<210> 6
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 <212> PRT
 <213> Homo sapiens

<400> 6

Asp	Ile	Gln	Leu	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly
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Asp	Arg	Val	Thr	Met	Ser	Cys	Lys	Ser	Ser	Gln	Ser	Val	Leu	Tyr	Ser
		20						25					30		

Ala	Asn	His	Lys	Asn	Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys
		35					40					45			

Ala	Pro	Lys	Leu	Leu	Ile	Tyr	Trp	Ala	Ser	Thr	Arg	Glu	Ser	Gly	Val
	50					55					60				

Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Phe	Thr
65					70					75					80

Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	Ile	Ala	Thr	Tyr	Tyr	Cys	His	Gln
				85					90					95	

Tyr	Leu	Ser	Ser	Trp	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Gln	Ile	Lys
				100				105					110		

Arg

<210> 7
 <211> 348
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (1)..(348)
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<400> 7
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 1 5 10 15
 tca gtg aag gtc tcc tgc aag gct tct ggc tac acc ttt act agc tac 96
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 20 25 30
 tgg ctg cac tgg gtc agg cag gca cct gga cag ggt ctg gaa tgg att 144
 Trp Leu His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45
 gga tac att aat cct agg aat gat tat act gag tac aat cag aac ttc 192
 Gly Tyr Ile Asn Pro Arg Asn Asp Tyr Thr Glu Tyr Asn Gln Asn Phe
 50 55 60
 aag gac aag gcc aca ata act gca gac gaa tcc acc aat aca gcc tac 240
 Lys Asp Lys Ala Thr Ile Thr Ala Asp Glu Ser Thr Asn Thr Ala Tyr
 65 70 75 80
 atg gag ctg agc agc ctg agg tct gag gac acg gca ttt tat ttt tgt 288
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Phe Tyr Phe Cys
 85 90 95
 gca aga agg gat att act acg ttc tac tgg ggc caa ggc acc acg gtc 336
 Ala Arg Arg Asp Ile Thr Thr Phe Tyr Trp Gly Gln Gly Thr Thr Val
 100 105 110
 acc gtc tcc tcg 348
 Thr Val Ser Ser
 115

<210> 8
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 8
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 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Leu His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Asn Pro Arg Asn Asp Tyr Thr Glu Tyr Asn Gln Asn Phe
50 55 60

Lys Asp Lys Ala Thr Ile Thr Ala Asp Glu Ser Thr Asn Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Phe Tyr Phe Cys
85 90 95

Ala Arg Arg Asp Ile Thr Thr Phe Tyr Trp Gly Gln Gly Thr Thr Val
100 105 110

Thr Val Ser Ser
115

<210> 9
<211> 116
<212> PRT
<213> Homo sapiens

<400> 9

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Trp Leu His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Asn Pro Arg Asn Asp Tyr Thr Glu Tyr Asn Gln Asn Phe
50 55 60

Lys Asp Lys Ala Thr Ile Thr Ala Asp Glu Ser Thr Asn Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Phe Tyr Phe Cys
85 90 95

Ala Arg Arg Asp Ile Thr Thr Phe Tyr Trp Gly Gln Gly Thr Thr Val
100 105 110

Thr Val Ser Ser
115

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<211> 149
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence

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tgacccagtg cagccagtag ctagtaaagg tgtagccaga agccttgcag gagaccttca 120
ctgatgaccc aggtttcttg acttcagcc 149

<210> 11
<211> 134
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic sequence

<400> 11
ccccagtaga acgtaatatc ccttgcacaa aaataaaatg ccgtgtcctc agacctcagg 60
ctgctcagct ccatgtaggc tgtattggtg gattcgtctg cagttattgt ggccttgtcc 120
ttgaagttct gatt 134

<210> 12
<211> 38
<212> DNA
<213> Unknown

<220>
<223> Primer

<400> 12
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<210> 13
 <211> 33
 <212> DNA
 <213> Unknown

 <220>
 <223> Primer

 <400> 13
 aagtggatcc tataatcatt cctaggatta atg 33

 <210> 14
 <211> 49
 <212> DNA
 <213> Unknown

 <220>
 <223> Primer

 <400> 14
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 <210> 15
 <211> 44
 <212> DNA
 <213> Unknown

 <220>
 <223> Primer

 <400> 15
 ggagacggtg accgtggtgc cttggcccca gtagaacgta gtaa 44

 <210> 16
 <211> 150
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic sequence

 <400> 16
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 ggccaagtag ttcttgtgat ttgcactgta taaaacactt tgactggact tacagctcat 120
 agtgacccta tctccaacag atgcgctcag 150

<210> 17
 <211> 52
 <212> DNA
 <213> Unknown

 <220>
 <223> Primer

 <400> 17
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 <210> 18
 <211> 45
 <212> DNA
 <213> Unknown

 <220>
 <223> Primer

 <400> 18
 agagaatcgc gaagggacac cagattccct agtggatgcc cagta 45

 <210> 19
 <211> 121
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic sequence

 <400> 19
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 caatgtcttc tggttgaaga gagctgatgg tgaaagtaaa atctgtccca gatccgctgc 120
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 <210> 20
 <211> 40
 <212> DNA
 <213> Unknown

 <220>
 <223> Primer

 <400> 20
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<210> 21
 <211> 33
 <212> DNA
 <213> Unknown

<220>
 <223> Primer

<400> 21
 gaccggcaga tctgcacctt ggtccctcca ccg 33

<210> 22
 <211> 339
 <212> DNA
 <213> Murinae gen. sp.

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 ataataaatt gccaggtctt caacttgtac tctgctgatg gtaagagtaa aatctgtccc 120
 agatccgctg cctgtgaagc gatcagggac accagattcc ctagtggatg ccagtagat 180
 cagcagttta ggagactgcc ctggtttctg ctggtaccag gccagtagt tcttgtgatt 240
 tgcactgtat aaaacacttt gactggactt acagctcata gtgacgtttt ctctgcaga 300
 cacagccaga gatgatggag actgggtcag ctgaatgtc 339

<210> 23
 <211> 348
 <212> DNA
 <213> Murinae gen. sp.

<400> 23
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 ggaggatttg tctgcagtca atgtggcctt gtccttgaag ttctgattgt actcagtata 180
 atcattccta ggattaatgt atccaatcca ttccagaccc tgtccaggcc tctgttttat 240
 ccagtgcagc cagtagctag taaaggtgta gccagaagcc ttgcaggaca tcttcactga 300
 ggccccaggt tttgacagtt cagcccctga ctctgcagc tggacctg 348

<210> 24
 <211> 339
 <212> DNA
 <213> Homo sapiens

<400> 24
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ataatatgtt gcaatgtctt ctggttgaag agagctgatg gtgaaagtaa aatctgtccc 120
agatccgctg ccagagaatc gcgaagggac accagattcc ctagtggatg ccagtagat 180
cagcagttta ggtgctttcc ctggtttctg ctggtaccag gccaaagtagt tcttgtgatt 240
tgcactgtat aaaacacttt gactggactt acagctcata gtgaccctat ctccaacaga 300
tgcgctcaga gatgatggag actgggtcag ctgaatgtc 339

<210> 25
<211> 348
<212> DNA
<213> Homo sapiens

<400> 25
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ggtggattcg tctgcagtta ttgtggcctt gtccttgaag ttctgattgt actcagtata 180
atcattccta ggattaatgt atccaatcca ttccagacct tgtccaggtg cctgcctgac 240
ccagtgcagc cagtagctag taaaggtgta gccagaagcc ttgcaggaga cttcactga 300
tgaccacaggt ttcttgactt cagccctga ttggaccagc tggacctg 348